

(1) GENERAL INFORMATION:

- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...21
- (D) OTHER INFORMATION: inosine

- (A) NAME/KEY: Other
- (B) LOCATION: 24...24
- (D) OTHER INFORMATION: A or C or G or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGMGGMANG AYTGGATHRT NGCNCC

26

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = Q or N

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = I or V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Trp Xaa Asp Trp Ile Xaa Ala Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...24
- (D) OTHER INFORMATION: inosine

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNTGGWSNG ARTGGATHAT NWGNCC

26

- (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Trp Ser Glu Trp Ile Ile Ser Pro  
1 5

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 9...9
- (D) OTHER INFORMATION: A or T or G or C

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ARRGTYTGNA CRATRGCRTG RTT

23

- (2) INFORMATION FOR SEQ ID NO:6:



- (A) NAME/KEY: Other
- (B) LOCATION: 5...5
- (D) OTHER INFORMATION: Xaa = G or S or A

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = G or A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Val Xaa Xaa Cys Xaa Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 2...2
- (D) OTHER INFORMATION: Xaa = any aa

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = any aa

- (A) NAME/KEY: Other
- (B) LOCATION: 4...4
- (D) OTHER INFORMATION: Xaa = R or A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Xaa Xaa Xaa  
1

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

005749.051900  
006750.072450

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAAGAACGA	GTTATTTTCA	GCTGCTGACT	GGAGACGGTG	CACGTCTGGA	TACGAGAGCA	60
TTTCCACTAT	GGGACTGGAT	ACAAACACAC	ACCCGGCAGA	CTTCAAGAGT	TTCAGACTGA	120
GGAGAAAACC	TTTCCCTTCT	GCTGCTACTG	CTGCTGCCGC	TGCTTTTGAA	AGTCCACTTC	180
CTTTCATGGT	TTTTCTTGCC	AAACCAGAGG	CACCTTCGCT	GCTGCCGCTG	TTCTCTTTGG	240
TGTCATTGCT	CGGCTGGCCA	GAGGATGAGA	CTCCCCAAAC	TCCTCACTTT	CTTGCTTTGG	300
TACCTGGCTT	GGCTGGACCT	GGAATTCATC	TGCACTGTGT	TGGGTGCCCC	TGACTTGGGC	360
CAGAGACCCC	AGGGGTCCAG	GCCAGGATTG	GCCAAAGCAG	AGGCCAAGGA	GAGGCCCCCC	420
CTGGCCCGGA	ACGTCTTCAG	GCCAGGGGGT	CACAGCTATG	GTGGGGGGGC	CACCAATGCC	480
AATGCCAGGG	CAAAGGGAGG	CACCGGGCAG	ACAGGAGGCC	TGACACAGCC	CAAGAAGGAT	540
GAAACCAAAA	AGCTGCCCCC	CAGACCGGGC	GGCCCTGAAC	CCAAGCCAGG	ACACCCTCCC	600
CAAAACAAGG	AGGCTACAGC	CCGGAAGTGT	ACCCCAAAAG	GACAGCTTCC	CGGAGGCAAG	660
GCACCCCCAA	AAGCAGGATC	TGTCCCCAGC	TCCTTCCTGC	TGAAGAAGGC	CAGGGAGCCC	720
GGGCCCCCAC	GAGAGCCCCA	GGAGCCGTTT	CGCCACCCCC	CCATCACACC	CCACGAGTAC	780
ATGCTCTCGC	TGTACAGGAC	GCTGTCCGAT	GCTGACAGAA	AGGGAGGCAA	CAGCAGCGTG	840
AAGTTGGAGG	CTGGCCTGGC	CAACACCATC	ACCAGCTTTA	TTGACAAAGG	GCAAGATGAC	900
CGAGGTCCCG	TGGTCAGGAA	GCAGAGGTAC	GTGTTTGACA	TTAGTGCCCT	GGAGAAGGAT	960
GGGCTGCTGG	GGGCCGAGCT	GCGGATCTTG	CGGAAGAAGC	CCTCGGACAC	GGCCAAGCCA	1020
GCGGTCCCCC	GGAGCCGGCG	GGCTGCCCAG	CTGAAGCTGT	CCAGCTGCCC	CAGCGGCCGG	1080
CAGCCGGCCG	CCTTGCTGGA	TGTGCGCTCC	GTGCCAGGCC	TGGACGGATC	TGGCTGGGAG	1140
GTGTTTCGACA	TCTGGAAGCT	CTTCCGAAAC	TTTAAGAACT	CGGCCAGCT	GTGCCTGGAG	1200
CTGGAGGCCT	GGGAACGGGG	CAGGACCGTG	GACCTCCGTG	GCCTGGGCTT	CGACCGCGCC	1260
GCCCCGGCAGG	TCCACGAGAA	GGCCCTGTTC	CTGGTGTTTG	GCCGCACCAA	GAAACGGGAC	1320
CTGTTCTTTA	ATGAGATTAA	GGCCCGCTCT	GGCCAGGACG	ATAAGACCGT	GTATGAGTAC	1380
CTGTTTCAGCC	AGCGGCGAAA	ACGGCGGGCC	CCATCGGCCA	CTCGCCAGGG	CAAGCGACCC	1440
AGCAAGAACC	TTAAGGCTCG	CTGCAGTCGG	AAGGCACTGC	ATGTCAACTT	CAAGGACATG	1500
GGCTGGGACG	ACTGGATCAT	CGCACCCCTT	GAGTACGAGG	CTTTCCACTG	CGAGGGGCTG	1560
TGCGAGTTCC	CATTGCGCTC	CCACCTGGAG	CCCACGAATC	ATGCAGTCAT	CCAGACCCTG	1620
ATGAACCTCGA	TGGACCCCGA	GTCCACACCA	CCCACCTGCT	GTGTGCCCAC	GCGGCTGAGT	1680
CCCATCAGCA	TCCTCTTCAT	TGACTCTGCC	AACAACGTGG	TGTATAAGCA	GTATGAGGAC	1740
ATGGTCGTGG	AGTCGTGTGG	CTGCAGGTAG	CAGCACTGGC	CCTCTGTCTT	CCTGGGTGGC	1800
ACATCCCAAG	AGCCCCTTCC	TGCACTCCTG	GAATCACAGA	GGGGTCAGGA	AGCTGTGGCA	1860
GGAGCATCTA	CACAGCTTGG	TGAAGGGATT	CAATAAGCTT	GCTCGCTCTC	TGAGTGTGAC	1920
TTGGGCTAAA	GGCCCCCTTT	TATCCACAAG	TTCCCCTGGC	TGAGGATTGC	TGCCCCTCTG	1980

CTGATGTGAC	CAGTGGCAGG	CACAGGTCCA	GGGAGACAGA	CTCTGAATGG	GA	CTGAGTCC	2040
CAGGAAACAG	TGCTTTCCGA	TGAGACTCAG	CCCACCATTT	CTCCTCACCT	GG	GCCCTTCTC	2100
AGCCTCTGGA	CTCTCCTAAG	CACCTCTCAG	GAGAGCCACA	GGTGCCACTG	CCT	CCTCAAA	2160
TCACATTTGT	GCCTGGTGAC	TTCCTGTCCC	TGGGACAGTT	GAGAAGCTGA	CT	GGGCAAGA	2220
GTGGGAGAGA	AGAGGAGAGG	GCTTGGATAG	AGTTGAGGAG	TGTGAGGCTG	TT	AGACTGTT	2280
AGATTTAAAT	GTATATTGAT	GAGATAAAAA	GCAAACTGT	GCCTAAAAAA	AAAA	AAAAAAA	2340
A							2341

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGCGTCCG	CCGAGCTGGG	CTCCGCCAAG	GGAATGCGAA	CGCGCAAGGA	AGGAAGGATG	60
CCGCGGGGCGC	CGAGAGAGAA	TGCCACGGCC	CGGGAGCCCC	TGGATCGCCA	GGAGCCCCCG	120
CCGAGGCCCGC	AGGAGGAGCC	CCAGCGGCGG	CCGCCACAGC	AGCCTGAAGC	TCGGGAGCCT	180
CCCCGSCAGGG	GCCCGCGCTT	GGTGCCCCAC	GAGTACATGC	TGTCAATCTA	CAGGACTTAC	240
TCCATCGCCG	AGAAGCTGGG	CATCAATGCT	AGCTTTTTC	AGTCTTCCAA	GTCGGCTAAT	300
ACGATCACTA	GCTTTGTAGA	CAGGGGACTA	GACGATCTCT	CGCACACTCC	TCTCCGGAGA	360
CAGAAATATT	TGTTTGATGT	GTCCACGCTC	TCAGACAAAG	AAGAGCTGGT	GGGCGCGGAC	420
GTGCGGCTGT	TTCGCCAGGC	GCCCGCTGCC	CTGGCGCCGC	CGGCGGCCGC	TCCGCTTGCA	480
GCTCTTCGCC	TGCCAGTCGC	CCCTGTGTGT	GGAAGCGCGG	AGCCTGGACC	CGCAGGGGCG	540
CCCCGGCCCCG	GCTGGGAAGT	CTTCGACGTG	TGGCGGGGCC	TGCGCCCCCA	GCCCTGGAAG	600
CAGCTGTGCT	TGGAGCTTCG	GGCCGCGTGG	GGCGGCGAGC	CGGGCGCCGC	GGAGGACGAG	660
GCGCGCACGC	CTGGGCCCCA	GCAGCCGCGG	CCCCCGGACC	TGCGGAGTCT	GGGCTTCGGC	720
CGGAGGGTGC	GGACCCCCCA	GGAGCGCGCC	TTGCTCGTCG	TGTTCTCCAG	GTCCCAGCGC	780
AAGACCTGT	TCGCCGAGAT	GCGCGAGCAG	CTGGGCTCGG	CGACCGAGGT	GGTCGGCCCC	840
GGTGTGTTGGG	CCGAGGGGTC	GGGGCCGCGG	CCGCCCGCCG	CGCCGCGCCG	GCCGTCGGGC	900
ACCCCGGACG	CTGGGCTCTG	GTCGCCCTCG	CCTGGCCGGC	GGCGGCGCAC	GGCCTTCGCC	960
AGCCGCCACG	GCAAGCGGCA	CGGCAAGAAG	TCGAGGCTGC	GCTGCAGCAA	GAAGCCCCTG	1020
CACGTGAACT	TCAAGGAGCT	GGGCTGGGAC	GACTGGATTA	TCGCGCCCCT	GGAGTACGAG	1080
GCCTACCACT	GCGAGGGCGT	GTGCGACTTC	CCGCTACGCT	CGCACCTGGA	GCCCACCAAC	1140
CACGCCATCA	TCCAGACGCT	GATGAACTCC	ATGGACCCCG	GCTCCACCCC	GCCCAGCTGC	1200
TGCGTGCCCA	CCAAATTGAC	TCCCATCAGC	ATCTTGTA	TCGACGCGGG	CAATAATGTG	1260
GTCTACAACG	AGTACGAGGA	GATGGTGGTG	GAGTCGTGCG	GCTGCAGG		1308

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Arg	Leu	Pro	Lys	Leu	Leu	Thr	Phe	Leu	Leu	Trp	Tyr	Leu	Ala	Trp
1				5					10					15	
Leu	Asp	Leu	Glu	Phe	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
			20					25					30		
Gln	Arg	Pro	Gln	Gly	Ser	Arg	Pro	Gly	Leu	Ala	Lys	Ala	Glu	Ala	Lys
		35					40					45			
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ser
	50					55					60				
Tyr	Gly	Gly	Gly	Ala	Thr	Asn	Ala	Asn	Ala	Arg	Ala	Lys	Gly	Gly	Thr
65					70					75					80
Gly	Gln	Thr	Gly	Gly	Leu	Thr	Gln	Pro	Lys	Lys	Asp	Glu	Pro	Lys	Lys
				85					90					95	
Leu	Pro	Pro	Arg	Pro	Gly	Gly	Pro	Glu	Pro	Lys	Arg	Gly	His	Pro	Pro
			100					105					110		
Gln	Thr	Arg	Gln	Ala	Thr	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu
	115						120					125			
Pro	Gly	Gly	Lys	Ala	Pro	Pro	Lys	Ala	Gly	Ser	Val	Pro	Ser	Ser	Phe
130						135					140				
Leu	Leu	Lys	Lys	Ala	Arg	Glu	Pro	Gly	Pro	Pro	Arg	Glu	Pro	Lys	Glu
145					150					155					160
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu
				165					170					175	
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val
		180					185					190			
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys
	195						200					205			
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Val	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe
210						215					220				
Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg
225					230				235						240
Ile	Leu	Arg	Lys	Lys	Pro	Ser	Asp	Thr	Ala	Lys	Pro	Ala	Val	Pro	Arg
			245						250					255	
Ser	Arg	Arg	Ala	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg
			260					265					270		
Gln	Pro	Ala	Ala	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly
	275						280					285			
Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys
	290					295					300				
Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg
305					310				315						320
Thr	Val	Asp	Leu	Arg	Gly	Leu	Gly	Phe	Asp	Arg	Ala	Ala	Arg	Gln	Val
			325						330					335	
His	Glu	Lys	Ala	Leu	Phe	Leu	Val	Phe	Gly	Arg	Thr	Lys	Lys	Arg	Asp
			340					345				350			
Leu	Phe	Phe	Asn	Glu	Ile	Lys	Ala	Arg	Ser	Gly	Gln	Asp	Asp	Lys	Thr
	355						360					365			
Val	Tyr	Glu	Tyr	Leu	Phe	Ser	Gln	Arg	Arg	Lys	Arg	Arg	Ala	Pro	Ser
	370					375					380				
Ala	Thr	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala	Arg	Cys
385					390					395					400



Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp  
 405 410 415  
 Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe Gly Cys Glu Gly Leu  
 420 425 430  
 Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val  
 435 440 445  
 Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr  
 450 455 460  
 Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp  
 465 470 475 480  
 Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu  
 485 490 495  
 Ser Cys Gly Cys Arg  
 500

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ala Ser Ala Glu Leu Gly Ser Ala Lys Gly Met Arg Thr Arg Lys  
 1 5 10 15  
 Glu Gly Arg Met Pro Arg Ala Pro Arg Glu Asn Ala Thr Ala Arg Glu  
 20 25 30  
 Pro Leu Asp Arg Gln Glu Pro Pro Pro Arg Pro Gln Glu Glu Pro Gln  
 35 40 45  
 Arg Arg Pro Pro Gln Gln Pro Glu Ala Arg Glu Pro Pro Gly Arg Gly  
 50 55 60  
 Pro Arg Leu Val Pro His Glu Tyr Met Leu Ser Ile Tyr Arg Thr Tyr  
 65 70 75 80  
 Ser Ile Ala Glu Lys Leu Gly Ile Asn Ala Ser Phe Phe Gln Ser Ser  
 85 90 95  
 Lys Ser Ala Asn Thr Ile Thr Ser Phe Val Asp Arg Gly Leu Asp Asp  
 100 105 110  
 Leu Ser His Thr Pro Leu Arg Arg Gln Lys Tyr Leu Phe Asp Val Ser  
 115 120 125  
 Thr Leu Ser Asp Lys Glu Glu Leu Val Gly Ala Asp Val Arg Leu Phe  
 130 135 140  
 Arg Gln Ala Pro Ala Ala Leu Ala Pro Pro Ala Ala Ala Pro Leu Ala  
 145 150 155 160  
 Ala Leu Arg Leu Pro Val Ala Pro Ala Ala Gly Ser Ala Glu Pro Gly  
 165 170 175  
 Pro Ala Gly Ala Pro Arg Pro Gly Trp Glu Val Phe Asp Val Trp Arg  
 180 185 190  
 Gly Leu Arg Pro Gln Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala

195                      200                      205  
 Ala Trp Gly Gly Glu Pro Gly Ala Ala Glu Asp Glu Ala Arg Thr Pro  
 210                      215                      220  
 Gly Pro Gln Gln Pro Pro Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly  
 225                      230                      235                      240  
 Arg Arg Val Arg Thr Pro Gln Glu Arg Ala Leu Leu Val Val Phe Ser  
 245                      250                      255  
 Arg Ser Gln Arg Lys Thr Leu Phe Ala Glu Met Arg Glu Gln Leu Gly  
 260                      265                      270  
 Ser Ala Thr Glu Val Val Gly Pro Gly Gly Gly Ala Glu Gly Ser Gly  
 275                      280                      285  
 Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Gly Thr Pro Asp Ala  
 290                      295                      300  
 Gly Leu Trp Ser Pro Ser Pro Gly Arg Arg Arg Arg Thr Ala Phe Ala  
 305                      310                      315                      320  
 Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser  
 325                      330                      335  
 Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp  
 340                      345                      350  
 Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys  
 355                      360                      365  
 Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile  
 370                      375                      380  
 Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys  
 385                      390                      395                      400  
 Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala  
 405                      410                      415  
 Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val Glu Ser  
 420                      425                      430  
 Cys Gly Cys Arg  
 435

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3...3
- (D) OTHER INFORMATION: Xaa = I or M or V

- (A) NAME/KEY: Other
- (B) LOCATION: 7...7
- (D) OTHER INFORMATION: Xaa = D or E

- (A) NAME/KEY: Other
- (B) LOCATION: 11...11
- (D) OTHER INFORMATION: Xaa = Y or F or H

- (A) NAME/KEY: Other
- (B) LOCATION: 16...16
- (D) OTHER INFORMATION: Xaa = L or V

- (A) NAME/KEY: Other
- (B) LOCATION: 18...18
- (D) OTHER INFORMATION: Xaa = D or E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Trp Ile Xaa Ala Pro Leu Xaa Tyr Glu Ala Xaa His Cys Glu Gly Xaa  
 1 5 10 15  
 Cys Xaa Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala His His Cys Ala Gly Val  
 1 5 10 15  
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Asp  
 1 5 10 15

Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Asp  
 1 5 10 15  
 Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Ile Val Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Val  
 1 5 10 15  
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val  
 1 5 10 15  
 Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala

20

25

30

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5				10					15		
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5				10					15		
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp	Ile	Met	Ala	Pro	Leu	Asp	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Asp
1				5				10					15		
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val
1				5				10						15	
Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	
			20					25					30		

006750-6T842560